68. (Added) The transgenic plant cell according to claim 29, wherein the nucleic acid molecule is derived from a plant cell.

69. (Added) The transgenic plant cell according to claim 68, wherein the nucleic acid molecule is derived from a tomato plant cell.

70. (Added) The transgenic plant cell according to claim 29, wherein the nucleic acid molecule is selected from the group consisting of the nucleic acid molecule encoding the amino acid sequence of SEQ ID NO:2 and the nucleic acid molecule comprising the coding region of the nucleotide sequence of SEQ ID NO: 1.

71. (Added) The transgenic plant cell according to claim 29, wherein the nucleic acid molecule comprises at least 15 contiguous nucleotides of the nucleic acid molecule or a complementary strand thereof.

REMARKS

The Claim Amendments

Applicants have cancelled claims 1, 13-28, 36, 38, 39, 42-47, 49, and 51 without prejudice. Applicants have amended claims 29-31, 33-35, 37, 40, 41, 48, 50 and 52 and have added claims 62-71. Thus, claims 29-35, 37, 40, 41, 48, 50, 52 and 62-71 are pending.

Applicants have amended claims 29, 31, 35, 37, 40, 41 and 50 to correct improper multiple dependencies, or dependencies on cancelled claims. Applicants have

amended claims 33-35 to improve their form. Applicants have further amended claims 29, 31, 40, 50, and 52 to additionally recite nucleic acids with a percent sequence identity to the nucleic acid molecule coding for a polypeptide comprising the amino acid sequence of SEQ ID NO: 2 or the nucleic acid molecule comprising the coding region of the nucleotide sequence of SEQ ID NO: 1. Support for these amendments is found in the specification at page 8, lines 7-9.

Applicants have added claims 62 and 63 to optionally include the subject matter of former multiple dependent claim 40. Applicants have added claim 64 to recite an isolated transgenic plant cell comprising a nucleic acid molecule with a percent sequence identity to the nucleic acid molecule coding for a polypeptide comprising the amino acid sequence of SEQ ID NO: 2 or the nucleic acid molecule comprising the coding region of the nucleotide sequence of SEQ ID NO: 1. Support for added claim 64 is found in the specification at page 8, lines 7-9. Finally, applicants have added claims 65-71 to recite the subject matter of former multiple dependent claim 29.

None of these amendments adds new matter. Their entry is requested.

The Restriction Requirement

The Examiner has stated that restriction of the claims into one of the following eleven groups is required under 35 U.S.C. § 121:

I. Claims 1 and 53-61, drawn to nucleic acids, vectors, hosts and methods of expression.

II. Claims 13, 14, 17, 18 and 49, drawn to proteins.

III. Claim 15, drawn to an antibody and methods of its use.

IV. Claims 16 and 50, drawn to antagonists and inhibitors.

V. Claims 22-26, drawn to methods of treatment.

VI. Claims 27, 28, 42, 43, drawn to transgenic animals.

VII. Claims 44-46, drawn to transgenic cells.

VIII. Claims 29-38, drawn to transgenic plants, plant cells, and plant tissue culture.

IX. Claims 40 and 41, drawn to transgenic organisms.

X. Claim 50, drawn to inhibition of gene expression using antisense.

XI. Claim 52, drawn to inhibition of gene expression using knockout constructs.

The Examiner states that claims 19-21 and 39 are generic to Groups I and II and that claims 19 and 20 are generic to Groups III and IV. The Examiner also states that claim 47 is generic to Groups VI and VII, claim 48 is generic to Groups VI and VIII, and claim 51 is generic to Groups III and IV. The Examiner states that the generic claims will be examined to the extent that they are encompassed by the subject matter of the specific elected group.

Applicants traverse in part. They request that the claims of Groups VIII-XI be examined together, to the extent that Groups VIII, IX, X, and XI read on transgenic plants and transgenic plant cells.

The Manual of Patent Examining Procedure (MPEP) states that there are two criteria for a proper requirement of restriction between patentably distinct inventions. The first is that the inventions must be independent or distinct as claimed. The second is that there must be a serious burden on the Examiner if restriction is not required. The MPEP further states that "[i]f the search and examination of an entire application can be made without serious burden, the examiner must examine it on the merits, even though it includes claims to distinct or independent inventions." MPEP § 803. The Examiner has ignored the second criterion of this MPEP procedural rule.

The Examiner asserts that the inventions of groups VIII-XI have acquired a separate status in the art as shown by their different classification and divergent subject matter. Specifically, the Examiner contends that the invention of Group VIII, drawn to transgenic plants and plant cells, requires a different search from the other groups. The Examiner states that the inventions of IX, X, and XI require analysis strategies distinct from each other as well as from the other groups because the claims of Group IX are drawn to transgenic organisms, antagonists and inhibitors of heterologous gene expression, while Groups X and XI are drawn to inhibitory mechanisms of host cells by nucleic acids and proteins. The Examiner also states

that the inventions of Groups X and XI are distinct from each other because antisense and knockout constructs have different modes of operation and are structurally different.

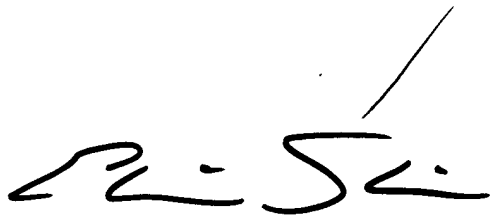
Applicants assert that there would be no serious burden for the Examiner to search the claims of Groups VIII-XI, to the extent that Groups VIII, IX, X, and XI read on transgenic plants and transgenic plant cells, because these searches are overlapping and essentially co-extensive. The subject matter of Group VIII requires a search of transgenic plant cells, plants and plant tissues comprising a nucleic acid molecule encoding the protein having SEQ ID NO: 2, a nucleic acid molecule having the nucleotide sequence of SEQ ID NO: 1, or a nucleic acid molecule that hybridizes to and shares sequence identity with or is a complementary strand of the aforementioned nucleic acids. Amended claims 40 and 41 of Group IX recite methods of inhibiting RNA-directed RNA synthesis by introducing the nucleic acid molecules recited in Group VIII into plant cells. Amended claims 50 and 52 of Groups X and XI recite methods of inhibiting gene expression in plant cells using antisense and knockout constructs, comprising introducing the nucleic acid molecules recited in Group VIII into plant cells. Thus, the subject matter of each of Groups IX-XI requires a search of plant cells comprising the nucleic acid molecules recited in Group VIII. Therefore, there would be no burden for the Examiner to search Groups VIII-XI together because the subject matter of Groups VIII-XI overlaps, such that a search for plant cells, plants and plant tissue comprising the nucleic acid molecules Group VIII would be co-extensive with a search for the methods of Groups IX-XI.

Accordingly, applicants request that Groups VIII-XI be rejoined, to the extent that the claims of groups IX-XI read on transgenic plants and transgenic plant cells.

Conclusion

If the Examiner does not agree with applicants' proposal to rejoin Groups VIII-XI, applicants provisionally elect with traverse the claims of Group VIII for initial substantive examination. 37 C.F.R. § 1.143. This election is made expressly without waiver of applicants' rights to continue to prosecute and to obtain claims to the non-elected and/or canceled subject matter either in this application or in other applications claiming priority herefrom.

Respectfully submitted,



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Appendix of Amendments

29. (Amended) [A] An isolated transgenic plant cell comprising a nucleic acid molecule stably integrated into the genome, wherein the nucleic acid molecule is:

(a) a nucleic acid molecule [of any one of claims 1 to 6 which is] encoding a polypeptide having the enzymatic activity of an RNA-directed RNA polymerase (RdRP) or encoding an enzymatically active fragment thereof, selected from the group consisting of:

(1) a nucleic acid molecule coding for a polypeptide comprising the amino acid sequence of SEQ ID NO: 2;

(2) a nucleic acid molecule comprising the coding region of the nucleotide sequence of SEQ ID NO: 1;

(3) a nucleic acid molecule that specifically hybridizes to a complementary strand of the nucleic acid molecule as defined in (1) or (2) in 0.25 M $NaHPO_4$ pH 7.2; 0.25 M NaCl, 7% SDS, 1 mM EDTA and 5-20% (w/v) polyethylene glycol (M_r 6-7.5x10^3) at 42° C for 4-24 hours;

(4) a nucleic acid molecule that has a sequence identity of at least 60% to the nucleic acid molecule of (1) or (2); and

(5) a nucleic acid molecule, the nucleotide sequence of which is degenerate as a result of the genetic code to a nucleotide sequence of the nucleic acid molecule as defined in (3) or (4);

wherein said nucleic acid molecule is linked to regulatory elements allowing transcription and/or expression of [the] said nucleic acid molecule in plant cells; and/or

(b) a template nucleic acid molecule [determined by the method of claim 18 which] coding for an RNA molecule that is capable of serving as a template for RNA-directed RNA synthesis, wherein said nucleic acid molecule is linked to regulatory elements allowing transcription of said nucleic acid molecule in plant cells.

30. (Amended) A transgenic plant comprising [plant cells] the plant cell [of claim 29] of any one of claims 29 or 65-71.

31. (Amended) [A] An isolated transgenic plant cell which contains stably integrated into the genome a nucleic acid molecule [of any one of claims 1 to 6 or a nucleic acid molecule of claim 7] selected from the group consisting of:

(1) a nucleic acid molecule coding for a polypeptide comprising the amino acid sequence of SEQ ID NO: 2;

(2) a nucleic acid molecule comprising the coding region of the nucleotide sequence of SEQ ID NO: 1;

(3) a nucleic acid molecule that specifically hybridizes to a complementary strand of the nucleic acid molecule as defined in (1) or (2) in 0.25 M $NaHPO_4$ pH 7.2; 0.25 M NaCl, 7% SDS, 1 mM EDTA and 5-20% (w/v) polyethylene glycol (M_r 6-7.5x10^3) at 42° C for 4-24 hours;

(4) a nucleic acid molecule that has a sequence identity of at least 60% to the nucleic acid molecule of (1) or (2);

(5) a nucleic acid molecule, the nucleotide sequence of which is degenerate as a result of the genetic code to a nucleotide sequence of the nucleic acid molecule as defined in (3) or (4); and

(6) a nucleic acid molecule comprising at least 15 contiguous nucleotides of any of (1) - (5) or a complementary strand thereof;

wherein said nucleic acid molecule [which] is linked to regulatory elements allowing transcription and/or expression of said nucleic acid molecule in plant cells[,]; and

wherein the presence, [of said nucleic acid molecules and/or the] transcription and/or expression of the nucleic acid molecule [of claim 7] leads to reduction of the synthesis of a polypeptide [of claim 13 or 14] having RNA-directed RNA polymerase (RdRP) activity in the [cells] cell.

33. (Amended) A transgenic plant comprising the plant [cells of] cell according to claim 31 or 32.

34. (Amended) A cultured plant tissue comprising [plant cells of claim] the plant cell according to any one of claims 29, 31 or 32.

35. (Amended) Harvestable parts of a plant [of claim 30] comprising [cells of claim] the plant cell according to any one of claims 29, 31 or 32.

37. (Amended) Propagation material of a plant [of claim 30,] comprising [cells of claim 29] the plant cell according to any one of claims 29, 31 or 32.

40. (Amended) [Use of the nucleic acid molecule of claim 7 or the vector of claim 8 or 9, or the antibody of claim 15 and/or the antagonist/inhibitor of claim 16 for] A method for inhibiting RNA-directed RNA synthesis in a plant cell comprising introducing into said plant cell a nucleic acid molecule of at least 15 nucleotides that specifically hybridizes in 0.25 M $NaHPO_4$ pH 7.2; 0.25 M NaCl, 7% SDS, 1 mM EDTA and 5-20% (w/v) polyethylene glycol (M_r 6-7.5x10^3) at 42° C for 4-24 hours to a nucleic acid molecule selected from the group consisting of:

(1) a nucleic acid molecule coding for a polypeptide comprising the amino acid sequence of SEQ ID NO: 2;

(2) a nucleic acid molecule comprising the coding region of the nucleotide sequence of SEQ ID NO: 1;

(3) a nucleic acid molecule that specifically hybridizes to a complementary strand of the nucleic acid molecule as defined in (1) or (2) in 0.25 M $NaHPO_4$ pH 7.2; 0.25 M NaCl, 7% SDS, 1 mM EDTA and 5-20% (w/v) polyethylene glycol (M_r 6-7.5x10^3) at 42° C for 4-24 hours;

(4) a nucleic acid molecule that has a sequence identity of at least 60% to the nucleic acid molecule of (1) or (2);

(5) a nucleic acid molecule, the nucleotide sequence of which is degenerate as a result of the genetic code to a nucleotide sequence of the nucleic acid molecule as defined in (3) or (4); and

(6) a nucleic acid molecule that is a complementary strand of (1)-(5).

41. (Amended) The [use] method of claim 40, 62 or 63, wherein said method ensures [for ensuring] stable heterologous gene expression in transgenic [organisms] plants.

48. (Amended) [A] The transgenic plant [or mammalian cells which contains stably integrated into the genome a] cell according to claim 29, wherein said nucleic acid

molecule [according to any one of claims 1 to 6 linked to regulatory elements which allow for expression of the nucleic acid molecule in plant or mammalian cells and wherein the nucleic acid molecule is foreign] is heterologous to the transgenic plant [or mammalian] cell [and optionally a template nucleic acid molecule].

50. (Amended) [Use of the nucleic acid molecule of any one of claims 1 to 6, a vector of claim 8 or 9 and/or a polypeptide of claim 13 or 14 and, optionally, an appropriate RdRP template nucleic acid molecule] A method for inhibiting expression of [any desired] a gene [by transferring the RdRP system to organisms that either lack a comparable mechanism or do not sufficiently express their own RdRP] in a plant cell, comprising stably integrating into the genome a nucleic acid molecule selected from group the group consisting of:

(1) a nucleic acid molecule coding for a polypeptide comprising the amino acid sequence of SEQ ID NO: 2;

(2) a nucleic acid molecule comprising the coding region of the nucleotide sequence of SEQ ID NO: 1;

(3) a nucleic acid molecule that specifically hybridizes to a complementary strand of the nucleic acid molecule as defined in (1) or (2) in 0.25 M $NaHPO_4$ pH 7.2; 0.25 M NaCl, 7% SDS, 1 mM EDTA and 5-20% (w/v) polyethylene glycol (M_r 6-7.5x10^3) at 42° C for 4-24 hours;

(4) a nucleic acid molecule that has a sequence identity of at least 60% to the nucleic acid molecule of (1) or (2);

(5) a nucleic acid molecule, the nucleotide sequence of which is degenerate as a result of the genetic code to a nucleotide sequence of the nucleic acid molecule as defined in (3) or (4); and

(6) a nucleic acid molecule coding for an RNA molecule that is capable of serving as a template for RNA-directed RNA synthesis wherein said nucleic acid molecule is linked to regulatory elements allowing transcription of said nucleic acid molecule in plant cells;

wherein said nucleic acid molecule may be optionally linked to regulatory elements allowing transcription and/or expression of said nucleic acid molecule in plant cells.

52. (Amended) A method to inhibit RNA-directed RNA polymerase activity [by destroying corresponding RdRP genes,] in a plant cell, comprising the step of producing a knock-out mutant in an RdRP gene, wherein said RdRP gene comprises a nucleic acid molecule selected from the group consisting of:

(1) a nucleic acid molecule coding for a polypeptide comprising the amino acid sequence of SEQ ID NO: 2;

(2) a nucleic acid molecule comprising the coding region of the nucleotide sequence of SEQ ID NO: 1;

(3) a nucleic acid molecule that specifically hybridizes to a complementary strand of the nucleic acid molecule as defined

in (1) or (2) in 0.25 M $NaHPO_4$ pH 7.2; 0.25 M NaCl, 7% SDS, 1 mM EDTA and 5-20% (w/v) polyethylene glycol (M_r 6-7.5x10^3) at 42° C. for 4-24 hours;

(4) a nucleic acid molecule that has a sequence identity of at least 60% to the nucleic acid molecule of (1) or (2); and

(5) a nucleic acid molecule, the nucleotide sequence of which is

degenerate as a result of the genetic code to a nucleotide sequence of the nucleic acid molecule as defined in (3) or (4).